

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Boyle, William J.
Lacey, David L.
Calzone, Frank J.
Chang, Ming-Shi

(ii) TITLE OF INVENTION: Osteoprotegerin

(iii) NUMBER OF SEQUENCES: 53

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.
(B) STREET: One Amgen Center Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 91362-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Winter, Robert B.
(C) REFERENCE/DOCKET NUMBER: A-378D5

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 124..1326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATCAAAGGCA GGGCATACTT CCTGTTGCCC AGACCTTATA TAAACGTCA TGTTGCCTG 60
GGCAGCAGAG AAGCACCTAG CACTGGCCCA GCGGCTGCCG CCTGAGGTTT CCAGAGGACC 120
ACA ATG AAC AAG TGG CTG TGC TGT GCA CTC CTG GTG TTC TTG GAC ATC 168
Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile
1 5 10 15

46

ATT Ile	GAA Glu	TGG Trp	ACA Thr	ACC Thr 20	CAG Gln	GAA Glu	ACC Thr	TTT Phe	CCT Pro 25	CCA Pro	AAA Lys	TAC Tyr	TTG Leu	CAT His 30	TAT Tyr	216
GAC Asp	CCA Pro	GAA Glu	ACC Thr 35	GGA Gly	CGT Arg	CAG Gln	CTC Leu	TTG Leu 40	TGT Cys	GAC Asp	AAA Lys	TGT Cys	GCT Ala 45	CCT Pro	GGC Gly	264
ACC Thr	TAC Tyr	CTA Leu 50	AAA Lys	CAG Gln	CAC His	TGC Cys	ACA Thr 55	GTC Val	AGG Arg	AGG Arg	AAG Lys	ACA Thr 60	CTG Leu	TGT Cys	GTC Val	312
CCT Pro	TGC Cys 65	CCT Pro	GAC Asp	TAC Tyr	TCT Ser	TAT Tyr 70	ACA Thr	GAC Asp	AGC Ser	TGG Trp	CAC His 75	ACG Thr	AGT Ser	GAT Asp	GAA Glu	360
TGC Cys 80	GTG Val	TAC Tyr	TGC Cys	AGC Ser	CCC Pro 85	GTG Val	TGC Cys	AAG Lys	GAA Glu 90	CTG Leu	CAG Gln	ACC Thr	GTG Val	AAA Lys	CAG Gln 95	408
GAG Glu	TGC Cys	AAC Asn	CGC Arg	ACC Thr 100	CAC His	AAC Asn	CGA Arg	GTG Val	TGC Cys 105	GAA Glu	TGT Cys	GAG Glu	GAA Glu	GGG Gly 110	CGC Arg	456
TAC Tyr	CTG Leu	GAG Glu 115	CTC Leu	GAA Glu	TTC Phe	TGC Cys	TTG Leu 120	AAG Lys	CAC His	CGG Arg	AGC Ser	TGT Cys	CCC Pro 125	CCA Pro	GGC Gly	504
TTG Leu	GGT Gly 130	GTG Val	CTG Leu	CAG Gln	GCT Ala	GGG Gly 135	ACC Thr	CCA Pro	GAG Glu	CGA Arg	AAC Asn	ACG Thr 140	GTT Val	TGC Cys	AAA Lys	552
AGA Arg	TGT Cys 145	CCG Pro	GAT Asp	GGG Gly	TTC Phe	TTC Phe 150	TCA Ser	GGT Gly	GAG Glu	ACG Thr	TCA Ser 155	TCG Ser	AAA Lys	GCA Ala	CCC Pro	600
TGT Cys 160	AGG Arg	AAA Lys	CAC His	ACC Thr	AAC Asn 165	TGC Cys	AGC Ser	TCA Ser	CTT Leu	GGC Gly 170	CTC Leu	CTG Leu	CTA Leu	ATT Ile	CAG Gln 175	648
AAA Lys	GGA Gly	AAT Asn	GCA Ala	ACA Thr 180	CAT His	GAC Asp	AAT Asn	GTA Val	TGT Cys 185	TCC Ser	GGA Gly	AAC Asn	AGA Arg	GAA Glu 190	GCA Ala	696
ACT Thr	CAA Gln	AAT Asn 195	TGT Cys	GGA Gly	ATA Ile	GAT Asp	GTC Val	ACC Thr 200	CTG Leu	TGC Cys	GAA Glu	GAG Glu	GCA Ala 205	TTC Phe	TTC Phe	744
AGG Arg	TTT Phe 210	GCT Ala	GTG Val	CCT Pro	ACC Thr	AAG Lys	ATT Ile 215	ATA Ile	CCG Pro	AAT Asn	TGG Trp	CTG Leu 220	AGT Ser	GTT Val	CTG Leu	792
GTG Val	GAC Asp 225	AGT Ser	TTG Leu	CCT Pro	GGG Gly	ACC Thr 230	AAA Lys	GTG Val	AAT Asn	GCA Ala	GAG Glu 235	AGT Ser	GTA Val	GAG Glu	AGG Arg	840
ATA Ile 240	AAA Lys	CGG Arg	AGA Arg	CAC His	AGC Ser 245	TCG Ser	CAA Gln	GAG Glu	CAA Gln	ACT Thr 250	TTC Phe	CAG Gln	CTA Leu	CTT Leu	AAG Lys 255	888

CTG TGG AAG CAT CAA AAC AGA GAC CAG GAA ATG GTG AAG AAG ATC ATC Leu Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile 260 265 270	936
CAA GAC ATT GAC CTC TGT GAA AGC AGT GTG CAA CGG CAT ATC GGC CAC Gln Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His 275 280 285	984
GCG AAC CTC ACC ACA GAG CAG CTC CGC ATC TTG ATG GAG AGC TTG CCT Ala Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro 290 295 300	1032
GGG AAG AAG ATC AGC CCA GAC GAG ATT GAG AGA ACG AGA AAG ACC TGC Gly Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys 305 310 315	1080
AAA CCC AGC GAG CAG CTC CTG AAG CTA CTG AGC TTG TGG AGG ATC AAA Lys Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys 320 325 330 335	1128
AAT GGA GAC CAA GAC ACC TTG AAG GGC CTG ATG TAC GCA CTC AAG CAC Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His 340 345 350	1176
TTG AAA GCA TAC CAC TTT CCC AAA ACC GTC ACC CAC AGT CTG AGG AAG Leu Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys 355 360 365	1224
ACC ATC AGG TTC TTG CAC AGC TTC ACC ATG TAC CGA TTG TAT CAG AAA Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys 370 375 380	1272
CTC TTT CTA GAA ATG ATA GGG AAT CAG GTT CAA TCA GTG AAG ATA AGC Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser 385 390 395	1320
TGC TTA TAGTTAGGAA TGGTCACTGG GCTGTTTCTT CAGGATGGGC CAACACTGAT Cys Leu 400	1376
GGAGCAGATG GCTGCTTCTC CGGCTCTTGA AATGGCAGTT GATTCCTTTC TCATCAGTTG	1436
GTGGGAATGA AGATCCTCCA GCCCAACACA CACACTGGGG AGTCTGAGTC AGGAGAGTGA	1496
GGCAGGCTAT TTGATAATTG TGCAAAGCTG CCAGGTGTAC ACCTAGAAAG TCAAGCACCC	1556
TGAGAAAGAG GATATTTTTTA TAACCTCAAA CATAGGCCCT TTCTTTCCTC TCCTTATGGA	1616
TGAGTACTCA GAAGGCTTCT ACTATCTTCT GTGTCATCCC TAGATGAAGG CCTCTTTTAT	1676
TTATTTTTTTT ATTCTTTTTT TCGGAGCTGG GGACCGAACC CAGGGCCTTG CGCTTGCGAG	1736
GCAAGTGCTC TACCACTGAG CTAAATCTCC AACCCCTGAA GGCCTCTTTC TTTCTGCCTC	1796
TGATAGTCTA TGACATTCTT TTTTCTACAA TTCGTATCAG GTGCACGAGC CTTATCCCAT	1856
TTGTAGGTTT CTAGGCAAGT TGACCGTTAG CTATTTTTCCT CTCTGAAGAT TTGATTGCGAG	1916
TTGCAGACTT GGCTAGACAA GCAGGGGTAG GTTATGGTAG TTTATTTAAC AGACTGCCAC	1976
CAGGAGTCCA GTGTTTCTTG TTCCTCTGTA GTTGACCTA AGCTGACTCC AAGTACATTT	2036
AGTATGAAAA ATAATCAACA AATTTTATTC CTTCTATCAA CATTGGCTAG CTTTGTTCCTA	2096

GGGCACTAAA AGAAACTACT ATATGGAGAA AGAATTGATA TTGCCCCCAA CGTTCAACAA 2156
 CCCAATAGTT TATCCAGCTG TCATGCCTGG TTCAGTGTCT ACTGACTATG CGCCCTCTTA 2216
 TTACTGCATG CAGTAATTCA ACTGGAAATA GTAATAATAA TAATAGAAAT AAAATCTAGA 2276
 CTCCATTGGA TCTCTCTGAA TATGGGAATA TCTAACTTAA GAAGCTTTGA GATTTTCAGTT 2336
 GTGTTAAAGG CTTTTATTAA AAAGCTGATG CTCTTCTGTA AAAGTTACTA ATATATCTGT 2396
 AAGACTATTA CAGTATTGCT ATTTATATCC ATCCAG 2432

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 401 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile
 1 5 10 15
 Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 20 25 30
 Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
 35 40 45
 Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
 50 55 60
 Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65 70 75 80
 Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu
 85 90 95
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
 100 105 110
 Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu
 115 120 125
 Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 130 135 140
 Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
 145 150 155 160
 Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys
 165 170 175
 Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr
 180 185 190
 Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 195 200 205

49

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val
 210 215 220
 Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 225 230 235 240
 Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 245 250 255
 Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln
 260 265 270
 Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala
 275 280 285
 Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly
 290 295 300
 Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys
 305 310 315 320
 Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 325 330 335
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu
 340 345 350
 Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr
 355 360 365
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu
 370 375 380
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
 385 390 395 400
 Leu

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 90..1292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTTATATAA ACGTCATGAT TGCCTGGGCT GCAGAGACGC ACCTAGCACT GACCCAGCGG 60
 CTGCCTCCTG AGGTTTCCCG AGGACCACA ATG AAC AAG TGG CTG TGC TGC GCA 113
 Met Asn Lys Trp Leu Cys Cys Ala
 1 5

50

CTC	CTG	GTG	CTC	CTG	GAC	ATC	ATT	GAA	TGG	ACA	ACC	CAG	GAA	ACC	CTT	161
Leu	Leu	Val	Leu	Leu	Asp	Ile	Ile	Glu	Trp	Thr	Thr	Gln	Glu	Thr	Leu	
	10					15					20					
CCT	CCA	AAG	TAC	TTG	CAT	TAT	GAC	CCA	GAA	ACT	GGT	CAT	CAG	CTC	CTG	209
Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Pro	Glu	Thr	Gly	His	Gln	Leu	Leu	
	25				30					35					40	
TGT	GAC	AAA	TGT	GCT	CCT	GGC	ACC	TAC	CTA	AAA	CAG	CAC	TGC	ACA	GTG	257
Cys	Asp	Lys	Cys	Ala	Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Val	
				45					50					55		
AGG	AGG	AAG	ACA	TTG	TGT	GTC	CCT	TGC	CCT	GAC	CAC	TCT	TAT	ACG	GAC	305
Arg	Arg	Lys	Thr	Leu	Cys	Val	Pro	Cys	Pro	Asp	His	Ser	Tyr	Thr	Asp	
			60					65					70			
AGC	TGG	CAC	ACC	AGT	GAT	GAG	TGT	GTG	TAT	TGC	AGC	CCA	GTG	TGC	AAG	353
Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	Val	Tyr	Cys	Ser	Pro	Val	Cys	Lys	
		75					80					85				
GAA	CTG	CAG	TCC	GTG	AAG	CAG	GAG	TGC	AAC	CGC	ACC	CAC	AAC	CGA	GTG	401
Glu	Leu	Gln	Ser	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	
	90					95					100					
TGT	GAG	TGT	GAG	GAA	GGG	CGT	TAC	CTG	GAG	ATC	GAA	TTC	TGC	TTG	AAG	449
Cys	Glu	Cys	Glu	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	
	105				110					115					120	
CAC	CGG	AGC	TGT	CCC	CCG	GGC	TCC	GGC	GTG	Val	GTG	CAA	GCT	GGA	ACC	497
His	Arg	Ser	Cys	Pro	Pro	Gly	Ser	Gly	Val	Gln	Ala	Gly	Thr	Pro		
				125					130					135		
GAG	CGA	AAC	ACA	GTT	TGC	AAA	AAA	TGT	CCA	GAT	GGG	TTC	TTC	TCA	GGT	545
Glu	Arg	Asn	Thr	Val	Cys	Lys	Lys	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Gly	
			140					145					150			
GAG	ACT	TCA	TCG	AAA	GCA	CCC	TGT	ATA	AAA	CAC	ACG	AAC	TGC	AGC	ACA	593
Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Ile	Lys	His	Thr	Asn	Cys	Ser	Thr	
		155					160					165				
TTT	GGC	CTC	CTG	CTA	ATT	CAG	AAA	GGA	AAT	GCA	ACA	CAT	GAC	AAC	GTG	641
Phe	Gly	Leu	Leu	Leu	Ile	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Val	
	170					175					180					
TGT	TCC	GGA	AAC	AGA	GAA	GCC	ACG	CAA	AAG	TGT	GGA	ATA	GAT	GTC	ACC	689
Cys	Ser	Gly	Asn	Arg	Glu	Ala	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	
	185				190					195					200	
CTG	TGT	GAA	GAG	GCC	TTC	TTC	AGG	TTT	GCT	GTT	CCT	ACC	AAG	ATT	ATA	737
Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	
				205					210					215		
CCA	AAT	TGG	CTG	AGT	GTT	TTG	GTG	GAC	AGT	TTG	CCT	GGG	ACC	AAA	GTG	785
Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Ser	Leu	Pro	Gly	Thr	Lys	Val	
			220					225					230			
AAT	GCC	GAG	AGT	GTA	GAG	AGG	ATA	AAA	CGG	AGA	CAC	AGC	TCA	CAA	GAG	833
Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	
		235					240					245				

CAA ACC TTC CAG CTG CTG AAG CTG TGG AAA CAT CAA AAC AGA GAC CAG Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Arg Asp Gln 250 255 260	881
GAA ATG GTG AAG AAG ATC ATC CAA GAC ATT GAC CTC TGT GAA AGC AGC Glu Met Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Ser Ser 265 270 275 280	929
GTG CAG CGG CAT CTC GGC CAC TCG AAC CTC ACC ACA GAG CAG CTT CTT Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu Gln Leu Leu 285 290 295	977
GCC TTG ATG GAG AGC CTG CCT GGG AAG AAG ATC AGC CCA GAA GAG ATT Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro Glu Glu Ile 300 305 310	1025
GAG AGA ACG AGA AAG ACC TGC AAA TCG AGC GAG CAG CTC CTG AAG CTA Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu Leu Lys Leu 315 320 325	1073
CTC AGT TTA TGG AGG ATC AAA AAT GGT GAC CAA GAC ACC TTG AAG GGC Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly 330 335 340	1121
CTG ATG TAT GCC CTC AAG CAC TTG AAA ACA TCC CAC TTT CCC AAA ACT Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe Pro Lys Thr 345 350 355 360	1169
GTC ACC CAC AGT CTG AGG AAG ACC ATG AGG TTC CTG CAC AGC TTC ACA Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His Ser Phe Thr 365 370 375	1217
ATG TAC AGA CTG TAT CAG AAG CTC TTT TTA GAA ATG ATA GGG AAT CAG Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln 380 385 390	1265
GTT CAA TCC GTG AAA ATA AGC TGC TTA TAACTAGGAA TGGTCACTGG Val Gln Ser Val Lys Ile Ser Cys Leu 395 400	1312
GCTGTTTCTT CA	1324

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 401 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile 1 5 10 15
Glu Trp Thr Thr Gln Glu Thr Leu Pro Pro Lys Tyr Leu His Tyr Asp 20 25 30
Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr 35 40 45

Tyr	Leu	Lys	Gln	His	Cys	Thr	Val	Arg	Arg	Lys	Thr	Leu	Cys	Val	Pro
50						55					60				
Cys	Pro	Asp	His	Ser	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
65					70					75					80
Val	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Ser	Val	Lys	Gln	Glu
				85					90					95	
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Glu	Glu	Gly	Arg	Tyr
			100					105					110		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Ser
		115					120					125			
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Lys
	130					135					140				
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys
145					150					155					160
Ile	Lys	His	Thr	Asn	Cys	Ser	Thr	Phe	Gly	Leu	Leu	Leu	Ile	Gln	Lys
				165					170					175	
Gly	Asn	Ala	Thr	His	Asp	Asn	Val	Cys	Ser	Gly	Asn	Arg	Glu	Ala	Thr
			180					185					190		
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg
		195					200					205			
Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val
	210					215					220				
Asp	Ser	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile
225					230					235					240
Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu
				245					250					255	
Trp	Lys	His	Gln	Asn	Arg	Asp	Gln	Glu	Met	Val	Lys	Lys	Ile	Ile	Gln
			260					265					270		
Asp	Ile	Asp	Leu	Cys	Glu	Ser	Ser	Val	Gln	Arg	His	Leu	Gly	His	Ser
		275					280					285			
Asn	Leu	Thr	Thr	Glu	Gln	Leu	Leu	Ala	Leu	Met	Glu	Ser	Leu	Pro	Gly
	290					295					300				
Lys	Lys	Ile	Ser	Pro	Glu	Glu	Ile	Glu	Arg	Thr	Arg	Lys	Thr	Cys	Lys
305					310					315					320
Ser	Ser	Glu	Gln	Leu	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn
				325					330					335	
Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	Tyr	Ala	Leu	Lys	His	Leu
			340					345					350		
Lys	Thr	Ser	His	Phe	Pro	Lys	Thr	Val	Thr	His	Ser	Leu	Arg	Lys	Thr
		355					360					365			
Met	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Arg	Leu	Tyr	Gln	Lys	Leu
	370					375					380				

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400

Leu

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 94..1296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTATATATAA CGTGATGAGC GTACGGGTGC GGAGACGCAC CGGAGCGCTC GCCCAGCCGC	60
CGCTCCAAGC CCCTGAGGTT TCCGGGGACC ACA ATG AAC AAG TTG CTG TGC TGC	114
Met Asn Lys Leu Leu Cys Cys	
1 5	
GCG CTC GTG TTT CTG GAC ATC TCC ATT AAG TGG ACC ACC CAG GAA ACG	162
Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr	
10 15 20	
TTT CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC TCT CAT CAG CTG	210
Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu	
25 30 35	
TTG TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA CAA CAC TGT ACA	258
Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr	
40 45 50 55	
GCA AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC CAC TAC TAC ACA	306
Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr	
60 65 70	
GAC AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC AGC CCC GTG TGC	354
Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys	
75 80 85	
AAG GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC ACC CAC AAC CGC	402
Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg	
90 95 100	
GTG TGC GAA TGC AAG GAA GGG CGC TAC CTT GAG ATA GAG TTC TGC TTG	450
Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu	
105 110 115	
AAA CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG CAA GCT GGA ACC	498
Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr	
120 125 130 135	

CCA	GAG	CGA	AAT	ACA	GTT	TGC	AAA	AGA	TGT	CCA	GAT	GGG	TTC	TTC	TCA	546
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	
				140					145					150		
AAT	GAG	ACG	TCA	TCT	AAA	GCA	CCC	TGT	AGA	AAA	CAC	ACA	AAT	TGC	AGT	594
Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	
			155					160					165			
GTC	TTT	GGT	CTC	CTG	CTA	ACT	CAG	AAA	GGA	AAT	GCA	ACA	CAC	GAC	AAC	642
Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	
		170					175					180				
ATA	TGT	TCC	GGA	AAC	AGT	GAA	TCA	ACT	CAA	AAA	TGT	GGA	ATA	GAT	GTT	690
Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	
	185					190					195					
ACC	CTG	TGT	GAG	GAG	GCA	TTC	TTC	AGG	TTT	GCT	GTT	CCT	ACA	AAG	TTT	738
Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Phe	
200					205					210					215	
ACG	CCT	AAC	TGG	CTT	AGT	GTC	TTG	GTA	GAC	AAT	TTG	CCT	GGC	ACC	AAA	786
Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	Lys	
				220					225					230		
GTA	AAC	GCA	GAG	AGT	GTA	GAG	AGG	ATA	AAA	CGG	CAA	CAC	AGC	TCA	CAA	834
Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	Gln	
			235					240					245			
GAA	CAG	ACT	TTC	CAG	CTG	CTG	AAG	TTA	TGG	AAA	CAT	CAA	AAC	AAA	GCC	882
Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Lys	Ala	
		250					255					260				
CAA	GAT	ATA	GTC	AAG	AAG	ATC	ATC	CAA	GAT	ATT	GAC	CTC	TGT	GAA	AAC	930
Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn	
	265					270					275					
AGC	GTG	CAG	CGG	CAC	ATT	GGA	CAT	GCT	AAC	CTC	ACC	TTC	GAG	CAG	CTT	978
Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu	
280					285					290					295	
CGT	AGC	TTG	ATG	GAA	AGC	TTA	CCG	GGA	AAG	AAA	GTG	GGA	GCA	GAA	GAC	1026
Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp	
				300					305					310		
ATT	GAA	AAA	ACA	ATA	AAG	GCA	TGC	AAA	CCC	AGT	GAC	CAG	ATC	CTG	AAG	1074
Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	Leu	Lys	
			315					320					325			
CTG	CTC	AGT	TTG	TGG	CGA	ATA	AAA	AAT	GGC	GAC	CAA	GAC	ACC	TTG	AAG	1122
Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	
		330					335					340				
GGC	CTA	ATG	CAC	GCA	CTA	AAG	CAC	TCA	AAG	ACG	TAC	CAC	TTT	CCC	AAA	1170
Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys	
	345					350					355					
ACT	GTC	ACT	CAG	AGT	CTA	AAG	AAG	ACC	ATC	AGG	TTC	CTT	CAC	AGC	TTC	1218
Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	
360					365					370					375	
ACA	ATG	TAC	AAA	TTG	TAT	CAG	AAG	TTA	TTT	TTA	GAA	ATG	ATA	GGT	AAC	1266
Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	
				380					385					390		

55

CAG GTC CAA TCA GTA AAA ATA AGC TGC TTA TAACTGGAAA TGGCCATTGA 1316
Gln Val Gln Ser Val Lys Ile Ser Cys Leu 400
395

GCTGTTTCCT CACAATTGGC GAGATCCCAT GGATGATAA 1355

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	1	5	10	15
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	20	25	30	
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	35	40	45	
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	50	55	60	
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	65	70	75	80
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	85	90	95	
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	100	105	110	
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	115	120	125	
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	130	135	140	
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	145	150	155	160
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	165	170	175	
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	180	185	190	
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	195	200	205	
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	210	215	220	
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	225	230	235	240

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Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
245 250 255
Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln
260 265 270
Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
275 280 285
Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
290 295 300
Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
305 310 315 320
Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
325 330 335
Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
340 345 350
Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
355 360 365
Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
370 375 380
Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys
385 390 395 400
Leu

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAGGAAGGA AAAAAGCGGC CGCTACAT

28

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
TCGACCCACG CGTCCG 16

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
CGGACGCGTG GG 12

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
TGTAACACGA CGGCCAGT 18

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
CAGGAAACAG CTATGACC 18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAATTAACCC TCACTAAAGG

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCATTATGAC CCAGAAACCG GAC

23

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGGTAGCGCC CTCCTCACA TTC

23

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GACTAGTCCC ACAATGAACA AGTGGCTGTG

30

59

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATAAGAATGC GGCCGCTAAA CTATGAAACA GCCCAGTGAC CATTC

45

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCCTCTAGAA AGAGCTGGGA C

21

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGCCGTGTTC CATTTATGAG C

21

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
ATCAAAGGCA GGGCATACTT CCTG 24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
GTTGCACTCC TGTTTCACGG TCTG 24

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
CAAGACACCT TGAAGGGCCT GATG 24

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
TAACTTTTAC AGAAGAGCAT CAGC 24

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

61

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCGCGGCCG CATGAACAAG TGGCTGTGCT GCG

33

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGCTCTAGAG AAACAGCCCA GTGACCATTC C

31

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTGAAGCTGT GCAAGAACCT GATG

24

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATCAAAGGCA GGCATACTT CCTG

24

62

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCCGTAAGAA ACAGCCCACT GACC

24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGATCCTGA AGCTGCTCAG TTG

24

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGCGCGGCCG CGGGGACCAC AATGAACAAG TTG

33

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
AGCTCTAGAA TTGTGAGGAA ACAGCTCAAT GGC 33

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
CCTCTGAGCT CAAGCTTCCG AGGACCACAA TGAACAAG 38

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
CCTCTGCGGC CGCTAAGCAG CTTATTTTCA CGGATTGAAC CTG 43

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
CCTCTGAGCT CAAGCTTCCG AGGACCACAA TGAACAAG 38

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

64

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCTCTGCGGC CGCTGTTGCA TTCCTTTCT G

31

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu	Thr	Leu	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Pro	Glu	Thr	Gly	His
1				5					10					15	

Gln Leu Leu

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TACGCACTGG ATCCTTATAA GCAGCTTATT TTTACTGATT GGAC

44

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
GTCCTCCTGG TACCTACCTA AAACAAC 27

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
TATGGATGAA GAAACTTCTC ATCAGCTGCT GTGTGATAAA TGTCCGCCGG GTAC 54

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
CCGGCGGACA TTTATCACAC AGCAGCTGAT GAGAAGTTTC TTCATCCA 48

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
1 5 10 15
Pro Gly Thr

66

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala	Leu	Leu	Val	Phe	Leu	Asp	Ile	Ile	Glu	Trp	Thr	Thr	Gln	Glu	Thr
1				5					10					15	
Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Pro	Glu	Thr	Gly	Arg	Gln	Leu
			20					25					30		
Leu	Cys	Asp	Lys	Cys	Ala	Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr
		35					40					45			
Val	Arg	Arg	Lys	Thr	Leu	Cys	Val	Pro	Cys	Pro	Asp	Tyr	Ser	Tyr	Thr
	50					55					60				
Asp	Ser	Trp	His	Thr	Ser										
65					70										

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

His	Ala	Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr	Ala	Pro	Glu	Pro
1				5					10					15	
Gly	Ser	Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	Met
			20					25					30		
Cys	Cys	Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys	Val	Phe	Cys	Thr
		35					40					45			
Lys	Thr	Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr	Thr
	50					55					60				
Gln	Leu	Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg	Cys
65					70				75						80
Ser	Ser	Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn	Arg
			85						90					95	

67

Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu
100 105 110

Gly Cys Arg Leu Cys Ala Pro Leu
115 120

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Tyr Leu His Tyr Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys
1 5 10 15

Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys
20 25 30

Thr Leu Cys Val Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His
35 40 45

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Tyr His Tyr Tyr Asp Gln Asn Gly Arg Met Cys Glu Glu Cys His Met
1 5 10 15

Cys Gln Pro Gly His Phe Leu Val Lys His Cys Lys Gln Pro Lys Arg
20 25 30

Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp
35 40 45

Asp Trp His
50

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Leu	Gly	Ile	Trp	Thr	Leu	Leu	Pro	Leu	Val	Leu	Thr	Ser	Val	Ala	
1			5					10					15			
Arg	Leu	Ser	Ser	Lys	Ser	Val	Asn	Ala	Gln	Val	Thr	Asp	Ile	Asn	Ser	
		20					25						30			
Lys	Gly	Leu	Glu	Leu	Arg	Lys	Thr	Val	Thr	Thr	Val	Glu	Thr	Gln	Asn	
		35				40						45				
Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His	Lys	Pro	Cys	Pro	
	50					55					60					
Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val	Asn	Gly	Asp	Glu	Pro	
65					70					75					80	
Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu	Tyr	Thr	Asp	Lys	Ala	His	
			85					90						95		
Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg	Leu	Cys	Asp	Glu	Gly	His	Gly	
			100				105						110			
Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr	Arg	Thr	Gln	Asn	Thr	Lys	Cys	Arg	
		115					120					125				
Cys	Lys	Pro	Asn	Phe	Phe	Cys	Asn	Ser	Thr	Val	Cys	Glu	His	Cys	Asp	
	130					135					140					
Pro	Cys	Thr	Lys	Cys	Glu	His	Gly	Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr	
145					150					155					160	
Ser	Asn	Thr	Lys	Cys	Lys	Glu	Glu	Gly	Ser	Arg	Ser	Asn	Leu	Gly	Trp	
			165						170					175		
Leu	Cys	Leu	Leu	Leu	Leu	Pro	Ile	Pro	Leu	Ile	Val	Trp	Val	Lys	Arg	
			180					185					190			
Lys	Glu	Val	Gln	Lys	Thr	Cys	Arg	Lys	His	Arg	Lys	Glu	Asn	Gln	Gly	
		195					200					205				
Ser	His	Glu	Ser	Pro	Thr	Leu	Asn	Pro	Glu	Thr						
	210					215										

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Gly	Leu	Ser	Thr	Val	Pro	Asp	Leu	Leu	Leu	Pro	Leu	Val	Leu	Leu	
1				5					10					15		
Glu	Leu	Leu	Val	Gly	Ile	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Leu	Val	Pro	
			20					25					30			
His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	
		35					40					45				
Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	
	50					55					60					
Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	
65					70					75					80	
Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	
				85					90					95		
Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	
			100					105					110			
Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	
		115					120					125				
Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	
	130					135					140					
Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	
145					150					155					160	
Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	
				165					170					175		
Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	
			180					185					190			
Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	
		195					200					205				
Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu	
						215						220				
Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys	
225					230					235					240	
Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu	
				245					250					255		

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr
275 280

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Leu	Arg	Leu	Ile	Ala	Leu	Leu	Val	Cys	Val	Val	Tyr	Val	Tyr	Gly	1	5	10	15
Asp	Asp	Val	Pro	Tyr	Ser	Ser	Asn	Gln	Gly	Lys	Cys	Gly	Gly	His	Asp	20	25	30	
Tyr	Glu	Lys	Asp	Gly	Leu	Cys	Cys	Ala	Ser	Cys	His	Pro	Gly	Phe	Tyr	35	40	45	
Ala	Ser	Arg	Leu	Cys	Gly	Pro	Gly	Ser	Asn	Thr	Val	Cys	Ser	Pro	Cys	50	55	60	
Glu	Asp	Gly	Thr	Phe	Thr	Ala	Ser	Thr	Asn	His	Ala	Pro	Ala	Cys	Val	65	70	75	80
Ser	Cys	Arg	Gly	Pro	Cys	Thr	Gly	His	Leu	Ser	Glu	Ser	Gln	Pro	Cys	85	90	95	
Asp	Arg	Thr	His	Asp	Arg	Val	Cys	Asn	Cys	Ser	Thr	Gly	Asn	Tyr	Cys	100	105	110	
Leu	Leu	Lys	Gly	Gln	Asn	Gly	Cys	Arg	Ile	Cys	Ala	Pro	Gln	Thr	Lys	115	120	125	
Cys	Pro	Ala	Gly	Tyr	Gly	Val	Ser	Gly	His	Thr	Arg	Ala	Gly	Asp	Thr	130	135	140	
Leu	Cys	Glu	Lys	Cys	Pro	Pro	His	Thr	Tyr	Ser	Asp	Ser	Leu	Ser	Pro	145	150	155	160
Thr	Glu	Arg	Cys	Gly	Thr	Ser	Phe	Asn	Tyr	Ile	Ser	Val	Gly	Phe	Asn	165	170	175	
Leu	Tyr	Pro	Val	Asn	Glu	Thr	Ser	Cys	Thr	Thr	Thr	Ala	Gly	His	Asn	180	185	190	
Glu	Val	Ile	Lys	Thr	Lys	Glu	Phe	Thr	Val	Thr	Leu	Asn	Tyr	Thr		195	200	205	

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Ala	Pro	Val	Ala	Val	Trp	Ala	Ala	Leu	Ala	Val	Gly	Leu	Glu	Leu	
1				5					10					15		
Trp	Ala	Ala	Ala	His	Ala	Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr	
			20					25					30			
Ala	Pro	Glu	Pro	Gly	Ser	Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	
		35					40					45				
Thr	Ala	Gln	Met	Cys	Cys	Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys	
	50					55					60					
Val	Phe	Cys	Thr	Lys	Thr	Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	
65					70					75					80	
Ser	Thr	Tyr	Thr	Gln	Leu	Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	
				85					90					95		
Gly	Ser	Arg	Cys	Ser	Ser	Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	
			100					105					110			
Glu	Gln	Asn	Arg	Ile	Cys	Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	
		115					120					125				
Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	
	130					135					140					
Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	
145					150					155					160	
Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	
				165					170					175		
Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	
			180					185					190			
Asn	Ala	Ser	Arg	Asp	Ala	Val	Cys	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	
		195					200					205				
Met	Ala	Pro	Gly	Ala	Val	His	Leu	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	
	210					215					220					
Gln	His	Thr														
225																

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Gly	Ala	Gly	Ala	Thr	Gly	Arg	Ala	Met	Asp	Gly	Pro	Arg	Leu	Leu	
1				5					10					15		
Leu	Leu	Leu	Leu	Leu	Gly	Val	Ser	Leu	Gly	Gly	Ala	Lys	Glu	Ala	Cys	
			20					25					30			
Pro	Thr	Gly	Leu	Tyr	Thr	His	Ser	Gly	Glu	Cys	Cys	Lys	Ala	Cys	Asn	
		35					40					45				
Leu	Gly	Glu	Gly	Val	Ala	Gln	Pro	Cys	Gly	Ala	Asn	Gln	Thr	Val	Cys	
	50					55					60					
Glu	Pro	Cys	Leu	Asp	Ser	Val	Thr	Phe	Ser	Asp	Val	Val	Ser	Ala	Thr	
65					70					75					80	
Glu	Pro	Cys	Lys	Pro	Cys	Thr	Glu	Cys	Val	Gly	Leu	Gln	Ser	Met	Ser	
				85					90					95		
Ala	Pro	Cys	Val	Glu	Ala	Asp	Asp	Ala	Val	Cys	Arg	Cys	Ala	Tyr	Gly	
			100					105					110			
Tyr	Tyr	Gln	Asp	Glu	Thr	Thr	Gly	Arg	Cys	Glu	Ala	Cys	Arg	Val	Cys	
		115					120					125				
Glu	Ala	Gly	Ser	Gly	Leu	Val	Phe	Ser	Cys	Gln	Asp	Lys	Gln	Asn	Thr	
	130					135					140					
Val	Cys	Glu	Glu	Cys	Pro	Asp	Gly	Thr	Tyr	Ser	Asp	Glu	Ala	Asn	His	
145					150					155					160	
Val	Asp	Pro	Cys	Leu	Pro	Cys	Thr	Val	Cys	Glu	Asp	Thr	Glu	Arg	Gln	
				165					170					175		
Leu	Arg	Glu	Cys	Thr	Arg	Trp	Ala	Asp	Ala	Glu	Cys	Glu	Glu	Ile	Pro	
			180					185					190			
Gly	Arg	Trp	Ile	Thr	Arg	Ser	Thr	Pro	Pro	Glu	Gly	Ser	Asp	Ser	Thr	
		195					200					205				
Ala	Pro	Ser	Thr	Gln	Glu	Pro	Glu	Ala	Pro	Pro	Glu	Gln	Asp	Leu	Ile	
	210					215					220					

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Tyr	Val	Trp	Val	Gln	Gln	Pro	Thr	Ala	Phe	Leu	Leu	Leu	Gly	Leu	1	5	10	15
Ser	Leu	Gly	Val	Thr	Val	Lys	Leu	Asn	Cys	Val	Lys	Asp	Thr	Tyr	Pro	20	25	30	
Ser	Gly	His	Lys	Cys	Cys	Arg	Glu	Cys	Gln	Pro	Gly	His	Gly	Met	Val	35	40	45	
Ser	Arg	Cys	Asp	His	Thr	Arg	Asp	Thr	Val	Cys	His	Pro	Cys	Glu	Pro	50	55	60	
Gly	Phe	Tyr	Asn	Glu	Ala	Val	Asn	Tyr	Asp	Thr	Cys	Lys	Gln	Cys	Thr	65	70	75	80
Gln	Cys	Asn	His	Arg	Ser	Gly	Ser	Glu	Leu	Lys	Gln	Asn	Cys	Thr	Pro	85	90	95	
Thr	Glu	Asp	Thr	Val	Cys	Gln	Cys	Arg	Pro	Gly	Thr	Gln	Pro	Arg	Gln	100	105	110	
Asp	Ser	Ser	His	Lys	Leu	Gly	Val	Asp	Cys	Val	Pro	Cys	Pro	Pro	Gly	115	120	125	
His	Phe	Ser	Pro	Gly	Ser	Asn	Gln	Ala	Cys	Lys	Pro	Trp	Thr	Asn	Cys	130	135	140	
Thr	Leu	Ser	Gly	Lys	Gln	Ile	Arg	His	Pro	Ala	Ser	Asn	Ser	Leu	Asp	145	150	155	160
Thr	Val	Cys	Glu	Asp	Arg	Ser	Leu	Leu	Ala	Thr	Leu	Leu	Trp	Glu	Thr	165	170	175	
Gln	Arg	Thr	Thr	Phe	Arg	Pro	Thr	Thr	Val	Pro	Ser	Thr	Thr	Val	Trp	180	185	190	
Pro	Arg	Thr	Ser	Gln	Leu	Pro	Ser	Thr	Pro	Thr	Leu	Val				195	200	205	

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met	Gly	Asn	Asn	Cys	Tyr	Asn	Val	Val	Val	Ile	Val	Leu	Leu	Leu	Val	1	5	10	15
Gly	Cys	Glu	Lys	Val	Gly	Ala	Val	Gln	Asn	Ser	Cys	Asp	Asn	Cys	Gln	20	25	30	

75

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Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
  35                                40                                45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys
  50                                55                                60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr
  65                                70                                75                                80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro
                        85                                90                                95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr
                100                                105                                110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn
                115                                120                                125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg
  130                                135                                140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro
  145                                150                                155                                160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu
                        165                                170                                175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu
                180                                185                                190

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(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

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Thr Ala Thr Gly Gly Ala Thr Gly Ala Ala Gly Ala Ala Ala Cys Thr
  1                                5                                10                                15

Thr Cys Thr Cys Ala Thr Cys Ala Gly Cys Thr Gly Cys Thr Gly Thr
                20                                25                                30

Gly Thr Gly Ala Thr Ala Ala Ala Thr Gly Thr Cys Cys Gly Cys Cys
  35                                40                                45

Gly Gly Gly Thr Ala Cys Ala Cys Cys Thr Ala Cys Thr Thr Cys Thr
  50                                55                                60

Thr Thr Gly Ala Ala Gly Ala Gly Thr Ala Gly Thr Cys Gly Ala Cys
  65                                70                                75                                80

Gly Ala Cys Ala Cys Ala Cys Thr Ala Thr Thr Thr Ala Cys Ala Gly
                85                                90                                95

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Gly Cys Gly Gly Cys Cys
100
